WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, October 13, 2005

Hide?	Set Name	Query	Hit Count
		DB=USPT; PLUR=YES; OP=OR	
☐	L1	oxygen.clm. same composition.clm.	8832
☐	L2	L1 same culture.clm. same media.clm.	7
☐	L3	L1 same portable.clm.	1
☐	L4	L1 same tank.clm.	13

END OF SEARCH HISTORY

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DATE: Thursday, October 13, 2005

Hide?	Set Name	Query	Hit Count
	DB=USPT; PLUR=YES; OP=OR		
☐	L1	winged.clm. same helix.clm. same regulator.clm.	0
☐	L2	winged.clm. same helix.clm.	2
☐	L3	l2 and agent.clm.	1
☐	L4	wingedhelix.clm.	0
☐	L5	winged-helix.clm.	0
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L6	winged-helix.clm.	1
☐	L7	l6 and inhibitor	1
☐	L8	l6 and inhibitor.clm.	1
☐	L9	winged-helix.ti,ab,clm. not l6 not l2	0
☐	L10	winged-helix same regulator	0
☐	L11	winged-helix same modulator	0
☐	L12	winged-helix same inhibitor	5
☐	L13	winged-helix same antagon$	0
☐	L14	winged-helix same down-regulator	0
☐	L15	winged-helix same repressor	0
☐	L16	winged-helix same suppressor	3

END OF SEARCH HISTORY

Service d'Exploration Fonctionnelle CardioRespiratoire Laboratoire de Physiologie GIP-Exercise, CHU Nord, Faculte de Medecine Jacques Lisfranc, Universite Jean Monnet, Saint-Etienne, France. Frederic.Roche@univ-st-etienne.fr

Pacing and clinical electrophysiology - PACE (United States) May 2002, 25 (5) p791-8, ISSN 0147-8389 Journal Code: 7803944

Publishing Model Print

Document type: Evaluation Studies; Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Ambulatory ECG had been proposed to examine the amplified high resolution signal-averaged electrocardiogram (SAECG). Clinical investigations are required to confirm the predictive value of such a high resolution technique in arrhythmic risk stratification. The prognostic value of ambulatory Holter SAECG was evaluated in 108 postinfarction patients for the purpose of predicting the occurrence of serious arrhythmic (**SARR**) events (sudden cardiac death [SCD], VT, or VF) in comparison with classical real-time SAECG. During the 42+/-8 months of follow-up, the sudden cardiac death mortality was 4.6% (five deaths), six (5.6%) patients had VT, and one (0.9%) VF. QRSd was found to be the most predictive parameter using ROC curves analysis for SAAR + outcome (W = 0.833 and W = 0.803 for 25-250 Hz and 40-250 Hz filters, respectively) followed by RMS (W = 0.766 and W = 0.721) and LAS (W = 0.759, W = 0.709) (all P < 0.01). Abnormal Holter SAECG for 25 and 40-Hz LP filter were significant predictors of **SARR** + by log-rank test (P < 0.01, P < 0.05, respectively). This study confirms that valuable prognostic information can be obtained from the ambulatory high resolution ECG technique and that Holter SAECG may predict arrhythmic risk in a postinfarction population.

Tags: Female; Male

Descriptors: *Arrhythmia--diagnosis--DI; *Electrocardiography, Ambulatory --methods--MT; *Myocardial Infarction--complications--CO; Action Potentials ; Aged; Arrhythmia--etiology--ET; Humans; Middle Aged; Prognosis; Prospective Studies; ROC Curve; Risk; Sensitivity and Specificity; Survival Analysis

Record Date Created: 20020606

Record Date Completed: 20030114

4/9/7

DIALOG(R)File 155:MEDLINE(R)

13971947 PMID: 11728861

Are the structures of SarA and SarR similar?

Cheung A L; Zhang G

Trends in microbiology (England) Dec 2001, 9 (12) p570-3, ISSN 0966-842X Journal Code: 9310916

Publishing Model Print

Document type: News

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Descriptors: *Bacterial Proteins--chemistry--CH; *Staphylococcus aureus --chemistry--CH; *Trans-Activators; Amino Acid Sequence; Bacterial Proteins --genetics--GE; Bacterial Proteins--metabolism--ME; Crystallization; Crystallography, X-Ray; Dimerization; Gene Expression Regulation, Bacterial ; Humans; Molecular Sequence Data; Protein Structure, Secondary; Staphylococcal Infections--microbiology--MI; Staphylococcus aureus

4/9/1
DIALOG(R)File 155:MEDLINE(R)

18364430 PMID: 16038790

Transcriptional profiles of regulatory and virulence factors of Staphylococcus aureus of bovine origin: oxygen impact and strain-to-strain variations.

Ster Celine; Gilbert Florence B; Cochard Thierry; Poutrel Bernard

Laboratoire de Pathologie Infectieuse et Immunologie, Institut National de la Recherche Agronomique, 37380 Nouzilly, France.

Molecular and cellular probes (England) Aug 2005, 19 (4) p227-35, ISSN 0890-8508 Journal Code: 8709751

Publishing Model Print-Electronic

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: In Process

Subfile: INDEX MEDICUS

Staphylococcus aureus is responsible for a large panel of infections in humans and animals. In cows, S. aureus provokes chronic intramammary infections. Little information is available about the regulation of virulence factors in bovine isolates. Moreover, oxygenation, which is low in an inflamed mammary gland, could play an important role during the infectious process. We investigated the impact of oxygen on regulatory and virulence factors transcription for three S. aureus bovine isolates cultivated in CYPG medium into a fermentor under moderate oxygenation or low oxygenation. A selective panel of regulatory factors and virulence factors was studied through their mRNA profiles by real-time PCR according to growth phases and oxygenation. RNAIII, rot and **sarR** genes, for the regulatory factors, and asp23 and cflA genes, for the virulence factors, were strongly expressed, whatever the oxygenation and the strains. Under low oxygenation, whatever the strain, an enhanced expression of srr, clfA and spa genes was detected. Some regulators such as sae, sarA and sigB were differentially transcribed according to the strain and the oxygenation condition. This study sustains the complexity of S. aureus genes global regulation and suggests the coexistence of different pathways that can be activated depending on the strain and the oxygen availability.

Record Date Created: 20050725

Date of Electronic Publication: 20050317

4/9/2
DIALOG(R)File 155:MEDLINE(R)

15314375 PMID: 15109784

Regulation of virulence determinants in Staphylococcus aureus: complexity and applications.

Bronner Stephane; Monteil Henri; Prevost Gilles

Institut de Bacteriologie, Faculte de Medecine, Universite Louis Pasteur - Hopitaux, Universitaires de Strasbourg, 3, rue Koeberle, F-67000 Strasbourg, France.

FEMS microbiology reviews (Netherlands) May 2004, 28 (2) p183-200, ISSN 0168-6445 Journal Code: 8902526

Publishing Model Print

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

promoter is dependent on the primary sigma factor sigmaSA, while that of the P3 promoter is dependent on sigmaSB. As determined by primer extension studies, the 5' end of the sigmaSB-initiated mRNA synthesized in vitro from the **sar** P3 promoter is in agreement with the 5' end of the cellular RNA.

Tags: Research Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--genetics--GE; *Bacterial Proteins --metabolism--ME; *Promoter Regions (Genetics); *Sigma Factor--metabolism --ME; * **Staphylococcus** aureus--genetics--GE; *Trans-Activators; *Transcription Factors--metabolism--ME; *Transcription, Genetic; Bacterial Proteins--isolation and purification--IP; Cloning, Molecular; DNA-Directed RNA Polymerases--metabolism--ME; Escherichia coli--genetics--GE; Operon; Sigma Factor--genetics--GE; Sigma Factor--isolation and purification--IP; Transcription Factors--genetics--GE; Transcription Factors--isolation and purification--IP

CAS Registry No.: 0 (Bacterial Proteins); 0 (SarA protein, bacterial) ; 0 (SigB protein, Bacteria); 0 (Sigma Factor); 0 (Trans-Activators); 0 (Transcription Factors)

Enzyme No.: EC 2.7.7.6 (DNA-Directed RNA Polymerases)

Record Date Created: 19971104

Record Date Completed: 19971104

7/9/6 (Item 6 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

11911694 PMID: 9190813

sar **Genetic determinants necessary for transcription of RNAII and RNAIII in the agr locus of** Staphylococcus **aureus.**

Cheung A L; Bayer M G; Heinrichs J H

Laboratory of Bacterial Pathogenesis and Immunology, Rockefeller University, New York, New York 10021, USA. cheunga@rockvax.rockefeller.edu

Journal of bacteriology (UNITED STATES) Jun 1997, 179 (12) p3963-71, ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: AI30061; AI; NIAID; AI37142; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

The temporal expression of most virulence factors in **Staphylococcus** aureus is regulated by pleiotropic loci such as agr and **sar** . We have previously shown that the **sar** locus affects hemolysin production because it is required for agr transcription. To delineate the **sar** genetic determinant required for agr transcription, single copies of fragments from the **sar** locus, encompassing the individual **sar** transcripts (**sarA** , sarC, and sarB), were introduced into a **sar** mutant via the integration vector pCL84. Although a DNA fragment encompassing the **sarA** transcript plus a 189-bp upstream region was sufficient for agr expression, complementation analysis revealed that the sarB transcript was the most effective in augmenting agr transcription as determined by RNAII and RNAIII transcription and gel retardation assays with the **P2** and P3 **promoters** of agr. As the region upstream of the **sarA** transcript encodes a 39-amino-acid open reading frame, ORF3, it is possible that posttranslational cooperation between the **sarA** gene product and ORF3 may be necessary for optimal agr expression. Deletion studies demonstrated that an intact **sarA** gene is essential for agr transcription. However, mutagenesis and in vitro translation studies revealed that unlike the agr locus, the required element is the **SarA** protein and not the RNA molecule.

13591988 PMID: 11159982

Characterization of sarR , a modulator of sar expression in Staphylococcus aureus.

Manna A; Cheung A L

Department of Microbiology, Dartmouth Medical School, Hanover, New Hampshire 03755, USA.

Infection and immunity (United States) Feb 2001, 69 (2) p885-96, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: AI30061; AI; NIAID; AI37182; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

The expression of virulence determinants in Staphylococcus aureus is controlled by global regulatory loci (e.g., sar and agr). The sar locus is composed of three overlapping transcripts (sar P1, P3, and P2 transcripts from P1, P3, and P2 promoters, respectively), all encoding the 372-bp sarA gene. The level of SarA, the major regulatory protein, is partially controlled by the differential activation of sar promoters. We previously partially purified a approximately 12 kDa protein with a DNA-specific column containing a sar P2 promoter fragment. In this study, the putative gene, designated sarR , was identified and found to encode a 13.6-kDa protein with homology to SarA. Transcriptional and immunoblot studies revealed the sarR gene to be expressed in other staphylococcal strains. Recombinant **SarR** protein bound sar P1, P2, and P3 promoter fragments in gel shift and footprinting assays. A **sarR** mutant expressed a higher level of P1 transcript than the parent, as confirmed by promoter green fluorescent protein fusion assays. As the P1 transcript is the predominant sar transcript, we confirmed that the **sarR** mutant expressed more SarA than the parental strain. We thus proposed that **SarR** is a regulatory protein that binds to the sar promoters to down-regulate P1 transcription and the ensuing SarA protein expression.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Gene Expression Regulation, Bacterial; *Genes, Regulator; *Staphylococcus aureus--genetics --GE; *Trans-Activators; Amino Acid Sequence; Antibodies, Monoclonal --biosynthesis--BI; Base Sequence; Binding Sites; Cloning, Molecular; Molecular Sequence Data; Promoter Regions (Genetics)

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Bacterial Proteins); 0 (SarA protein, bacterial); 0 (Trans-Activators)

Record Date Created: 20010222

Record Date Completed: 20010315

4/9/11

13053722 PMID: 11018457

Theoretical study of convergent ultrasound hyperthermia for treating bone tumors.

Lu B Y; Yang R S; Lin W L; Cheng K S; Wang C Y; Kuo T S

Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan, ROC.

Medical engineering & physics (ENGLAND) May 2000, 22 (4) p253-63,

4/9/9
DIALOG(R)File 155:MEDLINE(R)

13736236 PMID: 11381122
Crystal structure of the SarR protein from Staphylococcus aureus.
Liu Y; Manna A; Li R; Martin W E; Murphy R C; Cheung A L; Zhang G
National Jewish Medical and Research Center and Departments of Immunology and Pharmacology, School of Medicine, University of Colorado Health Science Center, 1400 Jackson Street, Denver, CO 80206; USA.
Proceedings of the National Academy of Sciences of the United States of America (United States) Jun 5 2001, 98 (12) p6877-82, ISSN 0027-8424

Journal Code: 7505876
Publishing Model Print-Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Subfile: INDEX MEDICUS
The expression of virulence determinants in Staphylococcus aureus is controlled by global regulatory loci (e.g., sarA and agr). The sar (Staphylococcus accessory regulator) locus is composed of three overlapping transcripts (sarA P1, P3, and P2, transcripts initiated from the P1, P3, and P2 promoters, respectively), all encoding the 124-aa SarA protein. The level of SarA, the major regulatory protein, is partially controlled by the differential activation of the sarA promoters. We previously partially purified a 13.6-kDa protein, designated **SarR**, that binds to the sarA promoter region to down-modulate sarA transcription from the P1 promoter and subsequently SarA expression. **SarR** shares sequence similarity to SarA, and another SarA homolog, SarS. Here we report the 2.3 A-resolution x-ray crystal structure of the dimeric **SarR**-MBP (maltose binding protein) fusion protein. The structure reveals that the **SarR** protein not only has a classic helix-turn-helix module for DNA binding at the major grooves, but also has an additional loop region involved in DNA recognition at the minor grooves. This interaction mode could represent a new functional class of the "winged helix" family. The dimeric **SarR** structure could accommodate an unusually long stretch of approximately 27 nucleotides with two or four bending points along the course, which could lead to the bending of DNA by 90 degrees or more, similar to that seen in the catabolite activator protein (CAP)-DNA complex. The structure also demonstrates the molecular basis for the stable dimerization of the **SarR** monomers and possible motifs for interaction with other proteins.
Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.
Descriptors: *Bacterial Proteins--chemistry--CH; *Staphylococcus aureus --chemistry--CH; *Trans-Activators; Amino Acid Sequence; Crystallization; DNA--metabolism--ME; Dimerization; Molecular Sequence Data
Molecular Sequence Databank No.: PDB/1HSJ
CAS Registry No.: 0 (Bacterial Proteins); 0 (SarA protein, bacterial); 0 (Trans-Activators); 9007-49-2 (DNA)
Record Date Created: 20010606
Record Date Completed: 20010628
Date of Electronic Publication: 20010529

4/9/10
DIALOG(R)File 155:MEDLINE(R)